Amendments to the Specification:

Replace the paragraph beginning at page 1, line 4, as with the following amended paragraph:

This is a divisional of U.S. Application Serial No.09/839,479, filed April 20, 2001 and issued as U.S. Patent No. 6,727,222, which is a divisional of U.S. Application Serial No. 09/418,710, filed October 15, 1999 and issued as U.S. Patent No. 6,596,482, which is a continuation-in-part of PCT/JP98/01783, filed April 17, 1999, and claims priority from Japanese Application Nos. 9/116570, filed April 18, 1997, and 9/310027, filed October 24, 1997.

Replace the paragraph beginning at page 17, line 11, as with the following amended paragraph:

As used herein, "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches are performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to a reference polypeptide. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. These programs are available at the web site of the National Center for Biotechnology Information.

Replace the paragraph beginning at page 26, line 9, as with the following amended paragraph:

Several sorts of sequence motifs characterized by the nuclear proteins were identified at 11 sites by employing the PSORT program (available at the PSORT WWW Server) utilizing a wide variety of conserved nuclear localization sequences.

Replace the paragraph beginning at page 26, line 15, as with the following amended paragraph:

Primers B SEQ ID NO:6/AACACAAGTGAAGCAAAAGCTGGA and M SEQ ID NO:7/GTGGTGTGCTAACTTGGTCCACAT (obtained from the 3' end of the gene) were used to amplify DNA obtained from each of the 24 monochromosomes of human/rodent somatic cell lines available from Coriell Cell Respositories, New Jersey (Dubois, B. L. and Naylor, S. (1993), Genomics, 16:315-319). The expected product of 111 bp was amplified only from GM10479, a monochromosomal cell line for human chromosome 14 (see FIG. 2A). Primers B (SEQ ID NO:6) and M (SEQ ID NO:7) were subsequently used for PCR onto a GeneBridge 4 radiation hybrid panel (Research Genetics, Huntsville, Ala.). The binary codes generated by assessing whether each hybrid is positive or negative for amplification were compared with the analogous codes for the markers constituting a framework map, using the server located at the web site of the Whitehead Institute for Biomedical Research/MIT Center for Genome Research. This step was repeated using primers W: SEQ ID NO:8/CCCATCGTGAGTCAAGAGT- GTCTGT and X: SEQ ID NO:9/CTCGCTTCTACCTTTTTATTGGCT (from the 5' end of the gene). Based on the pattern obtained from this panel by identifying the amplification in the panel, BAZ was proved to be located on the 14 q between the two markers D14S730 and D14S75 (see FIG. 2B).

Replace the paragraph beginning at page 33, line 4, as with the following amended paragraph:

To locate BAZ2α on the chromosome, PCR primers D (SEQ ID NO:17/TTGCCGTATTTGGCTGGTATC) and E (SEQ ID

NO:18/CATAGAGAAGAGGGCAGGGTTGA), which amplify a fragment of 132 bp, were used to amplify the DNA from each of the 24 monochromosomes of human/rodent somatic cell lines (Dubois, B. L. and Naylor, S. (1993), Genomics, 16:315-319) obtained from Coriell Cell Respositories (New Jersey). The BAZ2α-containing region was identified using 91 GeneBridge 4 radiation hybrid panels (Walter M. A. et al., (1994), Nature Genetics, 7:22-28). These panels were screened by PCR using primers D and E again. The binary codes generated by assessing whether each hybrid is positive or negative for markers constituting a framework map, using the server located at the web site of the Whitehead Institute for Biomedical Research/MIT Center for Genome Research. BAZ2α was thus proved to be located 12q24.3-ter from D12S367 (see FIG. 7B).

Replace the paragraph beginning at page 35, line 26, as with the following amended paragraph:

The motifs of the protein encoded by the gene obtained were searched for in PROSITE. The proteins were compared using Bestfit from GCG. A nuclear transport signal was identified using the PSORT Server online.

Replace the paragraph beginning at page 37, line 12, as with the following amended paragraph:

To create a chromosome map of BAZ2β, primers nb7n (SEQ ID NO:25/TGTTGCTGCATCACTTGTGTAGTT) and NB7ee (SEQ ID NO:26/GGCATGACAATAATGTC- TGCAAA) were prepared and used to amplify the DNA obtained from each of the 24 human/rodent monochromosomal somatic cell lines (Dubois, B. L. and Naylor, S. (1993), Genomics, 16:315-319). The amplification of the 147 bp fragment as expected PCR product indicated that the gene was likely to be located on human monochromosome 2 (FIG. 11). The locus region of BAZ2β was determined by use of 91 radiation hybrid panels of GeneBridge 4 (Walter, M. A. et al., (1994), Nature Genetics, 7:22-28). The hybrid panels were screened by PCR using primers nb7n and nb7ee again. The binary codes

generated by assessing whether each hybrid is positive or negative for the amplification were compared with the analogous codes for the markers constituting a framework map, using the server located at the web site of the Whitehead Institute for Biomedical Research/MIT Center for Genome Research to identify the chromosomal locus of this gene. As a result, BAZ2β was confirmed to be located on chromosome 2q23-24 and between markers D2S1986 and G09369 (FIG. 11).

Replace the paragraph beginning at page 41, line 3, as with the following amended paragraph:

The motifs of the proteins encoded by BAZ1βS and BAZ1βL genes were searched in PROSITE. The proteins were compared using a MAP program of a BCM search launcher available online) under the default setting conditions; the outpour results were edited using a box shade program. A nuclear transport signal was identified using the PSORT Server online.

Replace the paragraph beginning at page 42, line 19, as with the following amended paragraph:

To create a chromosome map of BAZ1β, primers nb3S (SEQ ID NO:35/GAAACGGGAGGAGCTGAAAAAG) and nb3T (SEQ ID NO:36/CCTTCAGGGGTATCCACCAA- TC) were prepared and used to amplify the DNA obtained from each of the 24 human/rodent monochromosomal somatic cell lines (Dubois, B. L. and Naylor, S. (1993), Genomics, 16:315-319). The expected PCR product of 156 bp was amplified from GM10791 from two distinct cell lines, suggesting that the BAZ1β gene is likely to be located on human chromosome 7 (FIG. 19A). The locus of BAZ1β was determined using 91 radiation hybrid panels of GeneBridge 4 (Walter, M. A. et al., (1994), Nature Genetics, 7:22-28). The hybrid panels were screened by performing PCR with primers nb3S and nb3T again. The locus of this gene was identified by comparing the binary codes generated by assessing each hybrid as positive or negative for the amplification with the analogous codes for the markers constituting a framework map using the server located at the web site of the Whitehead Institute

for Biomedical Research/MIT Center for Genome Research. As a result, BAZ1β was confirmed to be mapped on chromosome 7q11-22 and also located between the markers D7S489 and D7S669 (FIG. 19B).